IN THE SPECIFICATION:

Please amend page 6 – page 8, line 16 as follows:

"Figure 1 shows detection of the Ah receptor in Wild-Type and Mutant Hepa-1c1c7 cells.

Figure 2 shows a restriction map and location of cDNA clones.

Figure 3 shows Northern blot analysis of wild type and class I mutant Hepa 1c1c7 cells.

Figure 4 shows peptide mapping and amino acid sequencing of internal fragments generated by CNBr.

Figure 5 shows the alignment of the basic helix-loop-helix domains of Ah-receptor (AHR), Sim, and ARNT.

Figure 6A shows a partial restriction map and location of human Ah-receptor cDNA clones.

Figure 6B shows the amino acid sequence of the human Ah-receptor (Hu) (SEQ ID NO: 4) and comparison with the murine Ah-receptor (SEQ ID NO: 2). Also shown is the amino acid sequence of the DNA binding domain of the human Ah receptor protein (SEQ ID NO: 37) and comparison with the DNA binding domain of the murine Ah receptor protein (SEQ ID NO: 38). Finally, also shown is the amino acid sequence of the ligand binding domain of human Ah receptor protein (SEQ ID NO: 39) and comparison with the ligand binding domain of the murine Ah receptor protein (SEQ ID NO: 40).

Figure 7 shows the ligand binding of the murine and Ah receptors.

Figure 8A, 8B, and 8C show gel shift assays demonstrating the binding of Ah receptor (AhR)-ARNT heterodimers to DRE3.

Figure 9 shows deletion analysis of the human and murine Ah-receptors.

Figure 10 shows an example of a mammalian expression vector for human AhR.

Figure 11 shows an example of a receptor expression plasmid and a reporter plasmid.

Figure 12 shows a plasmid map of pSV.Sport1.

Figure 13 shows a plasmid map pSport M'Ahr.

Figure 14A, 14B, and 14C show the pharmacology of the Ah Receptor expressed in yeast. Figure 14A shows the structure of ligands used in the dose-response assay and the key to symbols. The square refers to ßNF, the triangle αNF, and the diamond, dexamethasone. Figure 14B shows the dose-response curves for AHR/ARNT/DRE-2 system. Cultures containing strain A303 transformed with plasmids pCWhuAHR, pY2ARNT, and pDRE23-Z were exposed to

agonist for 16-18 hours and ß-galactosidase assays performed to measure reporter activity; ß-Galactosidase units were converted to percent of the maximal activity of ßNF and plotted against concentration. Figure 14C shows the dose-response curve for the chimeric AHR-LexA signaling system. Strain GRS4 transformed with plasmids pEGAYRNΔ166 and pSH18-34 were grown in 2% galactose selection media containing agonists for 16-18 hours. ß-Galactosidase activity was measured to determine reporter gene expression. ß-Galactosidase units for all ligands were compared to the maximum response of ßNF and plotted against agonist concentrations.

Figure 15 shows a representative CAT assay of extracts from cells transfected with selected Gal4-fusion chimeras. The (-) means without ßNF, the (+) means with ßNF. Due to the high level of activity, extracts from the following plasmids were diluted 10-fold:pGAHRNΔ409, pGAHRCΔ418/VP, pGAHRNΔ520. Extracts from plasmids pGAHRNΔ409/CΔ165 and pGARNTNΔ581 were diluted 20-fold.

Figure 16 shows a schematic diagram of amino – carboxyl-terminal deletion GAL4-AHR fusion constructs and the average of their CAT assay results. The values reported are the average of two to four independent experiments with standard error never greater than 25%. The box marked GAL4 represents yeast GAL4 (1-147 amino acids) vertical bars represent the basic helix loop helix (bHLH) the stripped box represents the PAS domain with the "A" and "B" repeats indicated therein with black boxes; (2); box with left-to-right diagonal lines represents the glutamine-rich region (Q) and the gray shaded box corresponds to TAD of the herpes simplex virus VP16 protein (VP16). The positions of the PAS, ligand binding domina, and TAD are indicated with horizontal bars. Fold induction, reported in the bar graph on the right, is relative to the control pS6424. Bars with gray diagonal lines represent experiments without ßNF, and black bars are those with ßNF. Ligand-dependent induction is indicated to the right of bars when relevant."